

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 11.9318 Seconds

(Without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613b-4

Perfect score: 579
Sequence: 1 QDWLTFQKHLTNTRVDN.....TFCVTCENQAPVHFVGSHC 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544	94.0	104	2 A39035	ribonuclease-relat
2	283	48.9	111	2 A27121	ribonuclease-relat
3	279.5	48.3	111	1 JX0120	ribonuclease-relat
4	263.5	45.5	111	2 JX0085	pancreatic ribonuc
5	142	24.5	119	2 S41111	pancreatic ribonuc
6	123	21.2	124	1 NRUI	pancreatic ribonuc
7	120	20.7	125	1 A32474	angiogenin (valida
8	118	20.4	128	1 NRCPB	pancreatic ribonuc
9	117	20.2	128	1 NRCU	pancreatic ribonuc
10	116	20.0	124	1 NRMHK	pancreatic ribonuc
11	112.5	19.4	145	1 A35932	angiogenin precurs
12	111	19.2	128	1 NRKS	pancreatic ribonuc
13	110	19.0	125	1 B43825	angiogenin - rabbi
14	110	19.0	128	1 NRYV	pancreatic ribonuc
15	108.5	18.7	147	2 I52469	pancreatic ribonuc
16	108	18.7	124	1 NRCB	pancreatic ribonuc
17	108	18.7	124	1 NRCB	pancreatic ribonuc
18	108	18.7	124	1 JCS560	pancreatic ribonuc
19	108	18.7	150	1 NRB	pancreatic ribonuc
20	107	18.5	124	2 S08549	pancreatic ribonuc
21	106	18.3	147	1 NRMUG	ribonuclease - dom
22	105	18.1	124	1 NRSH	angiogenin precurs
23	105	18.1	124	1 NRP	pancreatic ribonuc
24	105	18.1	124	1 NRP	pancreatic ribonuc
25	105	18.1	124	2 S07141	pancreatic ribonuc
26	104.5	18.0	123	1 A43825	angiogenin - pig
27	104	18.0	124	1 NRM	pancreatic ribonuc
28	104	18.0	124	1 NRG	pancreatic ribonuc
29	103	17.8	124	1 NRGF	pancreatic ribonuc

30	103	17.8	124	1 NRP	pancreatic ribonuc
31	103	17.8	128	1 NRP	pancreatic ribonuc
32	103	17.8	167	2 S20066	pancreatic-type ri
33	102	17.6	128	1 NRHO	pancreatic ribonuc
34	101.5	17.5	155	2 JG6159	eosinophil-associa
35	100	17.3	124	1 NRGPA	pancreatic ribonuc
36	99	17.1	124	1 NRDEO	pancreatic ribonuc
37	99	17.1	124	1 NRCM	pancreatic ribonuc
38	99	17.1	124	1 NRCM	pancreatic ribonuc
39	99	17.1	124	1 NRCB	pancreatic ribonuc
40	98.5	17.0	124	2 S08546	pancreatic ribonuc
41	98	16.9	124	1 NRG	pancreatic ribonuc
42	98	16.9	156	2 JG6160	pancreatic ribonuc
43	97	16.8	124	1 NRANE	pancreatic ribonuc
44	96.5	16.7	119	2 JX0115	pancreatic ribonuc
45	96	16.6	124	1 NRAMT	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_Change 30-Jun-1993

C:Accession: A39035

R:Ridelt, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <AR>

C:Superfamily: pancreatic ribonuclease

Query Match 94.0%; Score 544; DB 2; Length 104;

Best Local Similarity 93.3%; Pred. No. 1.4e-47;

Matches 97; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY	1 QDWLTFQKHLTNTRVDNINLSTNLFHCKDKNTFYSPREPKAICKGIASKNVLT 60
DB	1 EDWLTFQKHLTNTRVDNINLSTNLFHCKDKNTFYSPREPKAICKGIASKNVLT 60
QY	61 FEFLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGSHC 104
DB	61 SEFLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGSHC 104

RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_Change 30-Jun-1993

C:Accession: A27121

R:Tritani, K.; Takio, K.; Kuwada, M.; Nitte, K.; Sakakibara, F.; Kawachi, H.; Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeian

A:Reference number: A27121; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TIT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: Lectin

Query Match 48.9%; Score 283; DB 2; Length 111;

Best Local Similarity 47.7%; Pred. No. 2.1e-21;

Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY	1 QDWLTFQKHLTNTRVDNINLSTNLF---HCKDKNTFYSPREPKAICKGIASKN 56
DB	1 ENWATFOCKHLINPIINCNTIMDNINIVYGQCKRVNTFISSATVKAICTGVI-NMN 59

A:Accession: A32474
 A:Molecule type: protein
 A:Residues: 1-125 <BN>
 A:Experimental source: plasma
 R:Maes, P.; Damart, D.; Kommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
 FEBS Lett. 241, 41-45, 1988
 A:Title: The complete amino acid sequence of bovine milk angiotensin.
 A:Reference number: S02001; MUID:89065101; PMID:3197838
 A:Accession: S02001
 A:Molecule type: protein
 A:Residues: 1-125 <MAE>
 A:Experimental source: milk
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 submitted to the Brookhaven Protein Data Bank, January 1995
 A:Reference number: A65065; PDB:1AG1
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
 A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
 A:Reference number: A58315; MUID:95224057; PMID:7708754
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 submitted to the Brookhaven Protein Data Bank, April 1996
 A:Reference number: A65709; PDB:1G10
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-125
 R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 Biochemistry 35, 8870-8880, 1996
 A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spect
 A:Reference number: A58821; MUID:96280645; PMID:8688423
 A:Contents: annotation; conformation by (1)H-NMR
 R:Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decotignies, J.P.; Spik, G.
 Eur. J. Biochem. 224, 811-822, 1994
 A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.
 A:Reference number: S48212; MUID:95010071; PMID:7925406
 A:Contents: annotation; conformation by (1)H-NMR
 C:Function: A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiotensin; hydrolase; nucleic acid degradation
 F:60-68/Region: receptor binding #status predicted
 F:14,41,115/active site: His, Lys, His #status predicted
 F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 20.7%; Score 120; DB 1; Length 125;
 Best Local Similarity 32.7%; Pred. No. 5.2e-05;
 Matches 32; Conservative 14; Mismatches 32; Indels 20; Gaps 5;

OY 16 DVDNNILSTNLF--HCKRKNFTIYSRPEVKAIC-----GIASKNVLTFFEFY 64
 DB 24 DEYCFMMKNNRRLTRPCKDRNFTIHGNKNDIKARNGRNGOPYRGDLRISKS-----EFO 78

OY 65 LSDC--NVTSR-PCRYKLKSTNFCVTCENQAPVHF 98
 DB 79 ITICKHKGSSRPCKRGATGDSRVIVCGENCLPVHF 116

RESULT 8
 NRCBP
 pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
 N:Alternate names: RNase IB
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
 C:Accession: A00826
 R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastera, W.; Beintema, J.J.
 Eur. J. Biochem. 75, 91-100, 1977
 A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
 A:Reference number: A91247; MUID:77185023; PMID:862624
 A:Accession: A00826
 A:Molecule type: protein
 A:Residues: 1-128 <VAN>
 A:Note: 64-Pro was also found
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted
 F:21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 20.4%; Score 118; DB 1; Length 128;
 Best Local Similarity 25.9%; Pred. No. 8.5e-05;
 Matches 30; Conservative 25; Mismatches 39; Indels 22; Gaps 7;

OY 4 LTFQKKHL-----TTRVDNENIL--STNLFHCKDKNTFIYSRPEVKAIC--KGII 52
 DB 6 MKFQROHMDPESPSNSV--CNVMMIRRMTOGRCKPNTVHESLADVOAQVCFQK 64

OY 53 ASKNVLTFFEFY----LSDCNVTSRP----CKYKLKSTNFCVTCENQ--APVHF 98
 DB 65 CKNGQTCYQSYSRMTITDCRVTSSSKFPCNSTRMSQAKSLIVACGPPYVHF 120

RESULT 9
 NRCU
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 C:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreat
 A:Reference number: A90612; MUID:77065676; PMID:9998936
 A:Accession: A00822
 A:Molecule type: protein
 A:Residues: 1-128 <VAN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.2%; Score 117; DB 1; Length 128;
 Best Local Similarity 28.2%; Pred. No. 0.00011;
 Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;

OY 6 FQKKHL-----TTRVDNENIL--STNLF--HCKRKNFTIYSRPEVKAICGIITASKNV 57
 DB 8 FERQHMDSRGSPTNENYCNEMKSRNMTQGRCKPVTFVHEPLADVOAQV----FQKNV 63

OY 58 L-----TTFEYLSDCNVTSRP----CKYKLKSTNFCVTCENQ--APVHF 98
 DB 64 LCKNGQTCYQSYSNMHTDCRVTSSNSDYPCNSTRMSQEKSLIVACGPNVYVHF 120

RESULT 10
 NRMHK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale
 N:Alternate names: RNase 1; RNase A
 C:Species: Balaenoptera acutirostrata (minke whale, lesser rorqual)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Welling, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.0%; Score 116; DB 1; Length 124;
 Best Local Similarity 26.9%; Pred. No. 0.00013;
 Matches 32; Conservative 16; Mismatches 43; Indels 28; Gaps 6;

[illegible]

RESULT: 11
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>.
A:Cross-references: GB:022516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide Bonds: #status predicted

RESULT 12

NRKS

pancreatic ribonuclease (EC 3.1.27.5) - castiagua

C:Species: *Proechimys guaitara* (castiagua)

C:Date: 17-Mar-1987 #sequence,revision 17-Mar-1987 #text,change 30-Sep-1993

C:Accession: A00821

R:Reintema, J.J., Knol, G., Martena, B.

Biochim. Biophys. Acta 705, 102-110, 1982

A:Title: The primary structures of pancreatic ribonucleases from African porcupine and c

A:Reference number: A90644; MUID:8300399; PMID:7115727

A:Accession: A00821

A:Molecule type: protein

A:Residues: 1-128 <BEI>

A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12-41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Blinding site: carboxylate (asn) (covalent) #status experimental

Best Local Similarity: 28.2%; Pred. No. 0.00043 37; Indels 28; Gaps 7.
Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7.

RESULT 13
B43825
angiotenin - rabbit
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Strýdom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiotenins: discet
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29833
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Note: submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

RESULT 14
NRY
pancreatic ribonuclease (EC 3.1.27.5) - cappybara
N:Alternate names: RNase 1; RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A008824
R:Beintema, J.-J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A008824
A:Molecule type: protein
A:Residues: 1-128

A:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; nucleic acid digestion; pancreas
E:12,41,119/Active site: His, Lys, His #status predicted
E:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Db 66 KNGOTNCYQSYSSNMHITDCRVTSNSKPEPDCSYRTTOAKSIVVACEGNTLVVPHF 120

RESULT 15

152489 ribonuclease 4 (EC 3.1.-.-) precursor - human

N:Alternate names: RNase 4

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 22-Jun-1999

C:Accession: 152489; S60163; S38272

R:Seno, M.; Futami, J.; Tsushima, Y.; Akita-gawa, K.; Kosaka, M.; Tada, H.; Yamada, H.

Biochim. Biophys. Acta 1261, 424-426, 1995

A:Title: Molecular cloning and expression of human ribonuclease 4 cDNA.

A:Reference number: 152489; PMID:95260866; PMID:7742370

A:Accession: 152489

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-147 <RES>

A:Cross-references: GB:D37931; NID:9976228; PIDN:BAA07150.1; PID:9976229

R:Rosenberg, H.F.; Dyer, K.D.

Nucleic Acids Res. 23, 4290-4295, 1995

A:Title: Human ribonuclease 4 (RNase 4): coding sequence, chromosomal localization and

A:Reference number: S60163; PMID:96091174; PMID:7501448

A:Accession: S60163

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 29-53; 'D', 55-147 <ROS>

A:Cross-references: EMBL:U36775; NID:91040977; PIDN:AAA96750.1; PID:91040978

R:Zhou, H.M.; Strydom, D.J.

Eur. J. Biochem. 217, 401-410, 1993

A:Title: The amino acid sequence of human ribonuclease 4, a highly conserved ribonuclease

A:Reference number: S38272; PMID:94039064; PMID:8223579

A:Accession: S38272

A:Molecule type: protein

A:Residues: 29-147 <ZHO>

C:Genetics:

A:Gene: GDB:RNASE4

A:Cross-references: GDB:6108046; OMIM:601030

A:Map position: 14q24-q31

A:Insertions: #status absent

C:Superfamily: pancreatic ribonuclease

C:Keywords: hydrolase

F:40,68,144/Active site: His, Lys, His #status predicted

F:53-109,67-120,85-135,92-99/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 31.2%; Score 108.5; DB 2; Length 147;

Matches 35; Conservative 16; Mismatches 44; Indels 17; Gaps 7;

QY 6 FOKKHL-----TNTRDVDCNNIL---STNLFHCKDKNTFIYSRPEPKAICK--GIASKN 56
 Db 36 FLRQHVHPEETGSDRCNLMQRRKMTLYHCKRFNFIHEDIMWINSICSTTNIOCKNG 95
 QY 57 VLTFEE--FYISDCNVT--SRP--CKYKLRKSTNTPFCVTCEN--QAPVHFWG 100
 Db 96 KMNCHGVVVTDCRDGTGSSRAPRCRYRAIASTRRVVIACGNGPQVPHFDG 147

Search completed: June 25, 2003, 14:58:01
 Job time : 15.9318 secs

